

Sequence 1: US6472518_8 Sequence 8 from Patent US 6472518 inClaims gi: 27289033
Length = 5416 (1 .. 5416)

Sequence 2: US20070219347_1 Sequence 1 Organism: Neisseria meningitidis
Length = 2242716 (1 .. 2242716)

Score = 8866 bits (4611), Expect = 0.0
Identities = 4984/5076 (98%), Gaps = 42/5076 (0%)
Strand=Plus/Plus

Query	6	GCATGCAAGCTGGAAGGAAACTTGCCGCAGCCAGGAAAACGGTGCAAGAGAGGGA	65
Sbjct	436931	GCATGCAAGCTGGAAGGAAACTTGCCGCAGCC-GGAAAACGGTGCAAGAGAGGGA	436989
Query	66	AGGGGGCGCGCGTTTGTGTGGCAAGATTGAAACGGTGGATTGAAAACAGCTTCTGAACAGG	125
Sbjct	436990	AGGGGGCGCGCGTTTGTGTGGCAAGATTGAAACGGTGGATTGAAAACAGCTTCTGAACAGG	437049
Query	126	TGGATTGCCGTTTGACAGGTGAGAAGTATTTTGCCAGCAGCAAGATACTTCTTATATAAT	185
Sbjct	437050	TGGATTGCCGTTTGACAGGTGAGAAGTATTTTGCCAGCAGCAAGATACTTCTTATATAAT	437109
Query	186	GAATAATAATTTATTTAAACCGTCTCTGAATGGGGCAGCAGGAGTTTTGAATGGAAT	245
Sbjct	437110	GAATAATAATTTATTTAAACCGTCTCTGAATGGGGCAGCAGGAGTTTTGAATGGAAT	437169
Query	246	TTGTTTACGACGTGGCAGAATCGGCAGTCAGCCCTGCGGTGATTAAAGTAATCGGCTTGG	305
Sbjct	437170	TTGTTTACGACGTGGCAGAATCGGCAGTCAGCCCTGCGGTGATTAAAGTAATCGGCTTGG	437229
Query	306	GCGGCGGCGGTTGCAATGCATCCAATAACATGGTTGCCAACAATGTGCGCGGTGTGGAGT	365
Sbjct	437230	GCGGCGGCGGTTGCAATGCATCCAATAACATGGTTGCCAACAATGTGCGCGGTGTGGAGT	437289
Query	366	TTATCAGTGCCAATACGGATGCGCAGTCTCTGGCAAAAAACCATGCGGCGAAGAGAATCC	425
Sbjct	437290	TTATCAGTGCCAATACGGATGCGCAGTCTCTGGCAAAAAACCATGCGGCGAAGAGAATCC	437349
Query	426	AGTTGGGTACGAATCTGACACGCGGTTTGGGCGCGGGCGGAATCCCGATATCGGCCGTG	485
Sbjct	437350	AGTTGGGTACGAATCTGACACGCGGTTTGGGCGCGGGCGGAATCCCGATATCGGCCGTG	437409
Query	486	CGGCAGCCCAGGAAGACCGGGAAGCCATTGAAGAAGCCATTTCGCGGTGCGAATATGCTGT	545
Sbjct	437410	CGGCAGCCCAGGAAGACCGGGAAGCCATTGAAGAAGCCATTTCGCGGTGCGAATATGCTGT	437469
Query	546	TTATCACGACCGGTATGGGCGGCGGTACCGGTACCGGTTCCGCGCCGGTTGTTGCTGAGA	605
Sbjct	437470	TTATCACGACCGGTATGGGCGGCGGTACCGGTACCGGTTCCGCGCCGGTTGTTGCTGAGA	437529
Query	606	TTGCCAAGTCTTTGGGCATTTGACCGTTGCCGTGGTTACCCGACCGTTTCGCATATGAAG	665
Sbjct	437530	TTGCCAAGTCTTTGGGCATTTGACCGTTGCCGTGGTTACCCGACCGTTTCGCATATGAAG	437589
Query	666	GTAAGCGCGTCCATGTGCGCACAGGCAGGGTTGGAACAGTTGAAAGAACACGTCGATTTCGC	725
Sbjct	437590	GTAAGCGCGTCCATGTGCGCACAGGCAGGGTTGGAACAGTTGAAAGAACACGTCGATTTCGC	437649
Query	726	TGATTATCATCCCGAACGACAAACTGATGACTGCATTTGGGTGAAGACGTAACGATGCGCG	785
Sbjct	437650	TGATTATCATCCCGAACGACAAACTGATGACTGCATTTGGGTGAAGACGTAACGATGCGCG	437709
Query	786	AAGCCTTCCGTGCCGCGCCGACAATGTATTGCGCGATGCGGTCGCAGGCATTTCCGAAGTGG	845
Sbjct	437710	AAGCCTTCCGTGCCGCGCCGACAATGTATTGCGCGATGCGGTCGCAGGCATTTCCGAAGTGG	437769
Query	846	TAACTTGCCCGAGCGAAATCATCAACCTCGACTTTGCCGACGTGAAAACCGTGATGAGCA	905
Sbjct	437770	TAACTTGCCCGAGCGAAATCATCAACCTCGACTTTGCCGACGTGAAAACCGTGATGAGCA	437829

Query	906	ACCGCGGTATCGCTATGATGGGTTTCGGGTTATGCCCAAGGTATCGACCGTGCGCGTATGG	965
Sbjct	437830	ACCGCGGTATCGCTATGATGGGTTTCGGGTTATGCCCAAGGTATCGACCGTGCGCGTATGG	437889
Query	966	CGACCGACCAGGCCATTTCCAGTCCGCTGCTGGACGATGTAACCTTGGACGGAGCGCGCG	1025
Sbjct	437890	CGACCGACCAGGCCATTTCCAGTCCGCTGCTGGACGATGTAACCTTGGACGGAGCGCGCG	437949
Query	1026	GTGTGCTGGTCAATATTACGACTGCTCCGGGTGCTTGAAAATGTCCGAGTTGTCCGAAG	1085
Sbjct	437950	GTGTGCTGGTCAATATTACGACTGCTCCGGGTGCTTGAAAATGTCCGAGTTGTCCGAAG	438009
Query	1086	TCATGAAAATCGTCAACCAAAGCGCGCATCCCGATTGGAATGCAAATTCGGTGCTGCTG	1145
Sbjct	438010	TCATGAAAATCGTCAACCAAAGCGCGCATCCCGATTGGAATGCAAATTCGGTGCTGCTG	438069
Query	1146	AAGACGAGACCATGAGCGAAGATGCCATCCGGATTACCATATCGCTACCGGTCTGAAAG	1205
Sbjct	438070	AAGACGAGACCATGAGCGAAGATGCCATCCGGATTACCATATCGCTACCGGTCTGAAAG	438129
Query	1206	AAAAAGGCGCGGTTCGATTTTGTTCCGGCAAGGGAGGTAGAAGCGGTTGCCCGTCCAAAC	1265
Sbjct	438130	AAAAAGGCGCGGTTCGATTTTGTTCCGGCAAGGGAGGTAGAAGCGGTTGCTCCGTCCAAAC	438189
Query	1266	AGGAGCAAAGCCACAATGTCTGAAGGTA-GATCCGCACCAATCGCGGTATCCGCACGATGA	1324
Sbjct	438190	AGGAGCAAAGCCACAATGTCTGAAGGTA-GATCCGCACCAATCGCGGTATCCGCACGATGA	438249
Query	1325	ACCTTACCGTTCGGGATTTTCGACAATCAGTCCGTACTTGACGAC-TTGAAATCCCTGCGA	1383
Sbjct	438250	ACCTTACCGTTCGGGATTTTCGACAATCAGTCCGTACTTGACGAC-TTGAAATCCCTGCGA	438309
Query	1384	TTTTCGCTCGTCAACACAATTCAGACAAATAATGTGCTGTTTGCCCGTAAACCTGCTGCC	1443
Sbjct	438310	TTTTCGCTCGTCAACACAATTCAGACAAATAATGTGCTGTTTGCCCGTAAACCTGCTGCC	438369
Query	1444	TCCCGAATCGGTTTGTCGGGTTTGGGAGGTATGTTTTCAAGATGTGCAATTTTCGTACG	1503
Sbjct	438370	TCCCGAATCGGTTTGTCGGGTTTGGGAGGTATGTTTTCAAGATGTGCAATTTTCGTACG	438429
Query	1504	GTTTGCGGTTCGGCGGATTCAGATTTTTCACCTTGATACAGACTTTCAGATATGGACACTT	1563
Sbjct	438430	GTTTGCGGTTCGGCGGATTCAGATTTTTCACCTTGATACAGACTTTCAGATATGGACACTT	438489
Query	1564	CAAAACAAACACTGTTGGACGGGATTTTAAAGCTGAAGGCAAACGGTACGACGGTGCGTA	1623
Sbjct	438490	CAAAACAAACACTGTTGGACGGGATTTTAAAGCTGAAGGCAAACGGTACGACGGTGCGTA	438549
Query	1624	CCGAGTTGATGGCGGGTTTGACAACCTTTTTCACGATGTGCTACATCGTTAATCGTCAAC	1683
Sbjct	438550	CCGAGTTGATGGCGGGTTTGACAACCTTTTTCACGATGTGCTACATCGTTAATCGTCAAC	438608
Query	1684	CCTCTGATTTTGGGCGAGACCGGCATGGATATGGGGCGGTATTCGTCGCTACCTGTATC	1743
Sbjct	438609	CCTCTGATTTTGGGCGAGACCGGCATGGATATGGGGCGGTATTCGTCGCTACCTGTATC	438668
Query	1744	GCGTCTGCCAATCGGCTGTTTGTATGGGTTTGTTCGGCAACTATCCGATTGCACTCGC	1803
Sbjct	438669	GCGTCTGCC-ATCGGCTGTTTGTATGGGTTTGTTCGGCAACTATCCGATTGCACTCGC	438727
Query	1804	ACCGGGGATGGGGCTGAATGCCTATTTACCTTTGCGGTCGTTAAGGGTATGGGC-TGCC	1862
Sbjct	438728	ACCGGGGATGGGGCTGAATGCCTATTTACCTTTGCGGTCGTTAAGGGTATGGGGCTGCC	438787
Query	1863	TTGGCAGGTTGCGTTGGGTGCGGTGTTTCATCTCCGGTCTGATTTTCATCCTGTTACGTT	1922
Sbjct	438788	TTGGCAGGTTGCGTTGGGTGCGGTGTTTCATCTCCGGTCTGATTTTCATCCTGTTACGTT	438847
Query	1923	TTTAAAGTCAGGGAAATGCT-GTCAACGCACTGCCTATGGGTTTGAAAATGTGCAATTGC	1981
Sbjct	438848	TTTAAAGTCAGGGAAATGCTGGTCAACGCACTGCCTATGGGTTTGAAAATGTGCAATTGC	438907

Query	1982	TGCCGGTATCGGTTTGTFTTTTGGCACTGATTTCCCTGAAAGGCGCAGGCCATTATCGTTG	2041
Sbjct	438908	TGCCGGTATCGGTTTGTFTTTTGGCACTGATTTCCCTGAAAGGCGCAGG-CATTATCGTTG	438966
Query	2042	CCAATCCGGCAACCTTGGTCGGTTTGGGCGATATTCATCAGCCGTCCGCGTTGTTGGCAC	2101
Sbjct	438967	CCAATCCGGCAACCTTGGTCGGTTTGGGCGATATTCATCAGCCGTCCGCGTTGTTGGCAT	439026
Query	2102	TGTTTCGGTTTGTCTATGGTGGTTCGATTTGGGACATTTCCGCGTTCAAGGCGCAA-CATCA	2160
Sbjct	439027	TGTTTCGGTTTGTCTATGGTGGTTCGATTTGGGACATTTCCGCGTTCAAGGCGCAATCATCA	439086
Query	2161	TCACCATCTTGACCATTACCGTCATTGCCAGCCTGATGGGTTTGAATGAATTTACGGCA	2220
Sbjct	439087	TCACCATCTTGACCATTACCGTCATTGCCAGCCTGATGGGTTTGAATGAATTTACGGCA	439146
Query	2221	TCATCGGCGAAGTACCGAGCATTGCGCCGACTTTTATGCAGATGGATTTTGAAGGCCCTGT	2280
Sbjct	439147	TCATCGGCGAAGTACCGAGCATTGCGCCGACTTTTATGCAGATGGATTTTGAAGGCCCTGT	439206
Query	2281	TTACCGTCAGC-TGGTCA--GTGATTTTCGTCTTCTTCTTGGTCGATCTATTTGACAGTA	2337
Sbjct	439207	TTACCGTCAGCATGGTCAGTGTGATTTTCGTCTTCTTCTTGGTCGATCTATTTGACAGTA	439266
Query	2338	CCGGAACGCTGGTCGGCATATCCACCGTGCCGGGCTGCTGGTGGACGGTAAGCTGCCCC	2397
Sbjct	439267	CCGGAACGCTGGTCGGCATATCCACCGTGCCGGGCTGCTGGTGGACGGTAAGCTGCCCC	439326
Query	2398	GCCTGAAACGCGCACTGCTTGCAGACTCTACCGCCATTATGGCAGGTGCGGCTTTGGGTA	2457
Sbjct	439327	GCCTGAAACGCGCACTGCTTGCAGACTCTACCGCCATTATGGCAGGTGCGGCTTTGGGTA	439386
Query	2458	CTTCTTCCACCACGCCCTTATGTGGAAGCGCGGGCGGTATCGGCAGGCGGACGGACCG	2517
Sbjct	439387	CTTCTTCCACCACGCCCTTATGTGGAAGCGCGGGCGGTATCGGCAGGCGGACGGACCG	439446
Query	2518	GCCTGACGGCGGTTACCGTCGGCGTATTGATGCTCGCCTGCCTGATGTTTTACCTTTGG	2577
Sbjct	439447	GCCTGACGGCGGTTACCGTCGGCGTATTGATGCTCGCCTGCCTGATGTTTTACCTTTGG	439506
Query	2578	CGAAAAGTGTTCCCGCTTTTGGCACCGCGCCCGCCCTGCTTTATGTGGCACGCAGATGC	2637
Sbjct	439507	CGAAAAGTGTTCCCGCTTTTGGCACCGCGCCCGCCCTGCTTTATGTGGCACGCAGATGC	439566
Query	2638	TCCGCAGTGCGAGGGATATTGATTGGGACGATATGACGGAAGCCGCACCCGCATTCTCTGA	2697
Sbjct	439567	TCCGCAGTGCGAGGGATATTGATTGGGACGATATGACGGAAGCCGCACCTGCGTTCTCTGA	439626
Query	2698	CCATTGTCTTCATGCCGTTTACCTATTTCGATTGCAGACGGCATCGCCTTCGGCTTCATCA	2757
Sbjct	439627	CCATTGTCTTCATGCCGTTTACTTATTTCGATTGCAGACGGCATCGCTTCGGCTTCATCA	439686
Query	2758	GCTATGCCGTGGTTAAACTTTTATGCCGCCGCACCAAAGACGTTCCGCCTATGGAATGGG	2817
Sbjct	439687	GTTATGCCGTGGTTAAACTTTTATGCCGCCGCACCAAAGACGTTCCGCCTATGGTATGGA	439746
Query	2818	TTGTTGCCGTATTGTGGGCACTGAAATTCTGGTATTTGGGCTGATTGATTTCGATATTAAA	2877
Sbjct	439747	TTGTTGCCGTATTGTGGGCACTGAAATTCTGGTATTTGGGCTGATTGATTTCGATATTAAA	439806
Query	2878	← ORF2 END AATGCCGTCTGAAAGGTTTTTCAGACGGCATTTTGTGTTGCCGATATA-TTAATTTTATTA	2936
Sbjct	439807	AATGCCGTCTGAAAGGTTTTTCAGACGGCATTTTGTGTTGCCGATATA-TTAATTTTATTA	439866
Query	2937	AATTATATAAAAAATCAAATACATAATAAAATACATCGGATTGCTTAAAAATAATACATTG	2996
Sbjct	439867	AATTATATAAAAAATCAAATACATAATAAAATACATCGGATTGCTTAAAAATAATACATTG	439926
Query	2997	TTTTTTATGTATAAAAAATTTTATAAGTTTTCAGGATTGATTATTGAAAAATTTTCTT	3056
Sbjct	439927	-TTTTTTATGTATAAAAAATTTTATAAGTTTTCAGGATTGATTATTCAAAAATTTTCTT	439985

Query	3057	GATTTCTGACAATTTTATTGAAACAAATAATTCAAAATTAATCTAGTTTAATCATAGAA	3116
Sbjct	439986	GATTTCTGACAATTTTATTGAAACAAATAATTCAAAATTAATCTAGTTTAATCATGGAA	440045
Query	3117	TTAAAATAAAATATTAAAATTATGTAATGAGTCTCCTTAAAAATGTTTGACATTTTCAGT	3176
Sbjct	440046	TTAAAATAAAATATTAAAATTATGTAATGAGTCTCCTTAAAAATGTTTGACATTTTCAGT	440105
Query	3177	CTTGTGTTTTAGATTATCGAAAAATAAACTACATAACACTACAAAGGAATATTACTATG	3236
Sbjct	440106	CTTGTGTTTTAGATTATCGAAAAATAAACTACATAACACTACAAAGGAACATTACTATG	440165
Query	3237	AAACCAATTCAGATGTTTTCCCTTTTCTGAATAATCCCCTTGTTTTCTCTGTCTGCG	3296
Sbjct	440166	AAACCAATTCAGATGTTTTCCCTTTTCTGAATAATCCCCTTGTTTTCTCTGTCTGCG	440225
Query	3297	GTTTTGCCGCATAATTCCGAACGGTCTGCTGTTTTTCTTTGATTTCGTTTTAAATATCAAT	3356
Sbjct	440226	GTTTTGCCGCATAATTCCGAACGGTCTGCTGTTTTTCTTTGATTTCGTTTTAAATATCAAT	440285
Query	3357	AAGATAATTTTTCCCATATATTTTTAATGATTGGATTGGGATGCCCGACGCGTCGGATGG	3416
Sbjct	440286	AAGATAATTTTTCCCATATATTTTTAATGATTGGATTGGGATGCCCGACGCGTCGGATGG	440345
Query	3417	CTGTGTTTTGCCGTCCGAATGTGATGGAAGCCTGTCCATACTGAAAAAAGTCTATAAAG	3476
Sbjct	440346	CTGTGTTTTGCCGTCCGAATGTGATGGAAGCCTGTCCATACTGAAAAAAGTCTATAAAG	440405
Query	3477	GAGAAATATGATGAGTCAACACTCTGCCGAGCACGTTTCCGCCAAGCCGTGAAAGAATC	3536
Sbjct	440406	GAGAAATATGATGAGTCAACACTCTGCCGAGCACGTTTCCGCCAAGCCGTGAAAGAATC	440465
Query	3537	GAATCCGCTTGCCGTCGCCGGTTGCGTCAATGCTTATTTTGACGATTGGCCACCCAAAG	3596
Sbjct	440466	GAATCCGCTTGCCGTCGCCGGTTGCGTCAATGCTTATTTTGACGATTGGCCACCCAAAG	440525
Query	3597	CGGTTTCAAAGCCATCTATCTGTCTGGCGGCGGCGTGGCAGCCTGTTCTTGCGGTATCCC	3656
Sbjct	440526	CGGTTTCAAAGCCATCTATCTGTCTGGCGGCGGCGTGGCAGCCTGTTCTTGCGGTATCCC	440585
Query	3657	TGATTTGGGCATTACCACAATGGAAGATGTGCTGATCGACGCACGACGATTACGGACAA	3716
Sbjct	440586	TGATTTGGGCATTACCACAATGGAAGATGTGCTGATCGACGCACGACGATTACGGACAA	440645
Query	3717	CGTGGATNCGCCTCTGCTGGTGGACATCGATGTGGGTGGGGCGGTGCATTCAATATTGC	3776
Sbjct	440646	CGTGGATACGCCTCTGCTGGTGGACATCGATGTGGGTGGGGCGGTGCATTCAATATTGC	440705
Query	3777	CCGTACCATTCGCAACTTTGAACGCGCCGGTGTTCAGCGGTTTACATCGAAGATCAGGT	3836
Sbjct	440706	CCGTACCATTCGCAACTTTGAACGCGCCGGTGTTCAGCGGTTTACATCGAAGATCAGGT	440765
Query	3837	AGCGCAAAAACGCTGCGGTCACCGTCCGAACAAAGCCATTGTTATCTNAAGATGNAATGG	3896
Sbjct	440766	AGCGCAAAAACGCTGCGGCCACCGTCCGAACAAAGCCATTG-TATCTAAAGATGAAATGG	440824
Query	3897	TCGACCGTATCAAAGCTGCCGTAGATGCGCGCGTTGNTGNGAACTTCGTGATTATGGCGC	3956
Sbjct	440825	TCGACCGTATCAAAGCTGCCGTAGATGCGCGCGTTGATGAGAACTTCGTGATTATGGCGC	440884
Query	3957	GTACCGATGCGCTGGCGGTAGAAGGTTTGGATGCCGCTATCGAACGCGCCCAAGCTTGTG	4016
Sbjct	440885	GTACCGATGCGCTGGCGGTAGAAGGTTTGGATGCCGCTATCGAACGCGCCCAAGCTTGTG	440944
Query	4017	TCGAAAGCCGCTGCGGACATGATTTTCCCTGAAGCCATGACCGATTGTAACATGTACCGC	4076
Sbjct	440945	TCG-AAGCCGCTGCGGACATGATTTTCCCTGAAGCCATGACCGATTGTAACATGTACCGC	441003
Query	4077	CAATTTGCAGATGCGGTGAAAAGTG--CGTGTGGCGGAACATTACCGAGTTTGGTTCCACT	4134
Sbjct	441004	CAATTTGCAGATGCGGTGAAAAGTGCCCGTGTGGCGGAACATTACCGAGTTTGGTTCCACT	441063

Query	4135	CCGCTTTATACCCAAAGCGAGCTGGCTGAAAACGGCGTGTGCTGGTGTATCCGCTG	4194
Sbjct	441064	CCGCTTTATACCCAAAGCGAGCTGGCTGAAAACGGCGTGTGCTGGTGTATCCGCTG	441123
Query	4195	TCATCGTTCCGTGCAGCAAGCAAAGCCGCTCTGAAATGTTTACGAAGCGATTATGCGCGAT	4254
Sbjct	441124	TCATCGTTCCGTGCAGCAAGCAAAGCCGCTCTGAAATGTTTACGAAGCGATTATGCGCGAT	441183
Query	4255	GGCACTCAGGCGGCGGTGGTGGACAGTATGCAAACCCGTGCCGAGCTGTACGAGCATCTG	4314
Sbjct	441184	GGCACTCAGGCGGCGGTGGTGGACAGTATGCAAACCCGTGCCGAGCTGTACGAGCATCTG	441243
Query	4315	AACTATCATGCCTTCGAGCAAAAACCTGGATAAAATGTTTCAAAAATGATTTACCGCTTTC	4374
Sbjct	441244	AACTATCATGCCTTCGAGCAAAAACCTGGATAAAATGTTTCAAAAATGATTTACCGCTTTC	441303
Query	4375	AGACGGTCTTTCAACAAATCCGCATCGGTGCTGAAAACCCGAAACCCATAAAAAACACA	4434
Sbjct	441304	AGACTGCCCTTTCAACAAATCCGCATCGGTGCTGAAAACCCGAAACCCATAAAAAACACA	441363
Query	4435	AAGGAGAAATACCATGACTGAAACTACTCAAACCCCGACCTTCAAACCTAAGAAATCCGT	4494
Sbjct	441364	AAGGAGAAATACCATGACTGAAACTACTCAAACCCCGACCTTCAAACCTAAGAAATCCGT	441423
Query	4495	TGCGCTTTTCAGGCGTTGCGGCCGTAATACCGCTTTGTGTACCGTTGGCCGCACCCGGCA	4554
Sbjct	441424	TGCGCTTTCTGGCGTTGCGGCCGTAATACCGCTTTGTGTACCGTTGGCCGTA-CCGGCA	441482
Query	4555	ACGATTTGGAGCTATCGCGGTTACGACATCTTGGATTTGGGCACAAAAATGC--GTTTGA	4612
Sbjct	441483	ACGATTT-GAGCTATCGCGGTTACGACATCTTGGATTT-GGCACAAAAATGCGAGTTTGA	441540
Query	4613	AGAAGTAGCCACCTGCTGATTACGGTCATCTGCCCAACAAATTCGACGTGGAAGCTTA	4672
Sbjct	441541	AGAAGTCGCCACCTGCTGATTACGGCCATCTGCCCAACAAATTCGAGCTGGCCGCTTA	441600
Query	4673	TAAAAGGAAGCTCAAATCCATGCGCGGCCTGCCTATCCGTGT-ATTAAAGTTTGGGAAA	4731
Sbjct	441601	TAAAACCAAGCTCAAATCCATGCGCGGCCTGCCTATCCGTGTGATTAAAGTTT-GGAAA	441659
Query	4732	GCCTGCCTGCACATACCCATCCGGATGGACGGTAATGGCGTACCGGCGGTATCCATGCTG	4791
Sbjct	441660	GCCTGCCTGCACATACCCATCC-GATGGAC-GTAAT-GCGTACCGGC-GTATCCATGCTG	441715
Query	4792	GGCTGCGTTCATCCCGAACGTGAAAGCCATCCCGGAAAGTGAAGCGCGGACATCGCCGA	4851
Sbjct	441716	GGCTGCGTTCATCCTGAACGTGAAAGCCAT-CCGGAAAGTGAAGCGCGGACATCGCCGA	441774
Query	4852	CAAACGTATG-CAGCCTCGG-AGCCTCCTGCTGTACTNNGGTATCAATA-TCGCACAACG	4908
Sbjct	441775	CAAACGTATCGCCAGCCTCGGCAGCATCCTCTTGTACT-GGTATCAATATTCGCACAACG	441833
Query	4909	GCAAACGCATTGA-GTTG-AAGCGACG-AGAGA-CATCGGCGGTCATTTCTGCAACTGT	4964
Sbjct	441834	GCAAACGCATTGAGGTTGAAAGCGACGAAGAGACCATCGGCGGTCATTTCTGCAACTGT	441893
Query	4965	TNCACGGC-AACGCCCAAGCG-ATCACACATCAAAGCCATGCACGTTTCACTGATTCTGT	5022
Sbjct	441894	TGCACGGCAAACGCCCAAGCGAATCACACATCAAAGCCATGCACGTTTCACTGATTCTGT	441953
Query	5023	ATG-CGAACACGAGTTCAACG-TTCTACCTTTACCG	5056
Sbjct	441954	ATGCCGAACACGAGTTCAACGCTTCTACCTTTACCG	441989